

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 2, 2006, 09:35:01 ; Search time 196 Seconds
(without alignments)
27.993 Million cell updates/sec

Title: US-10-570-233-1
Perfect score: 59
Sequence: 1 LKATTNSKLMMY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 960796

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	59	100.0	12	9	ADY73917	Ady73917 Transmiss
2	29	49.2	15	2	AAW73902	Aaw73902 B. forsyt
3	28	47.5	9	8	ADO34138	Ado34138 Human CLA
4	28	47.5	10	8	ADO34198	Ado34198 Human CLA
5	28	47.5	16	8	ADO34054	Ado34054 Human CLA
6	28	47.5	18	2	AAR53003	Aar53003 Example o
7	28	47.5	20	9	ADW52300	Adw52300 Human PL
8	27	45.8	15	9	ADY82781	Ady82781 Protein k
9	27	45.8	19	4	AAM19389	Aam19389 Peptide #
10	27	45.8	19	4	ABB38781	Abb38781 Peptide #
11	27	45.8	19	4	AAM32253	Aam32253 Peptide #

12	27	45.8	19	4	ABB23817	Abb23817 Protein #
13	27	45.8	19	4	AAM71978	Aam71978 Human bon
14	27	45.8	19	4	AAM59420	Aam59420 Human bra
15	27	45.8	19	4	ABG53662	Abg53662 Human liv
16	27	45.8	19	5	ABG41793	Abg41793 Human pep
17	27	45.8	20	9	AED42223	Aed42223 Human pro
18	26	44.1	12	6	ABR42329	Abr42329 Immunomod
19	26	44.1	12	7	ADC36105	Adc36105 Chemokine
20	26	44.1	12	8	ADR42853	Adr42853 Modulator
21	26	44.1	13	9	ADZ37998	Adz37998 Human kin
22	26	44.1	15	8	ADL21992	Adl21992 125P5C8 p
23	26	44.1	15	9	ADY82800	Ady82800 Protein k
24	26	44.1	16	5	AAM49540	Aam49540 TRAS1 Pol
25	26	44.1	17	9	ADY38558	Ady38558 Antigenic
26	26	44.1	18	2	AAR29952	Aar29952 TCR pepti
27	26	44.1	18	9	ADY64005	Ady64005 Human MCS
28	26	44.1	18	9	ADY64004	Ady64004 Human MCS
29	26	44.1	19	2	AAW76177	Aaw76177 Feline FL
30	26	44.1	19	7	ABM18906	Abm18906 S. pneumo
31	26	44.1	20	10	AEE38860	Aee38860 Human ser
32	25	42.4	10	4	ABP13660	Abp13660 HIV A02 s
33	25	42.4	10	7	ADE65194	Ade65194 Corticotr
34	25	42.4	10	7	ADE65189	Ade65189 Corticotr
35	25	42.4	10	7	ADE65192	Ade65192 Corticotr
36	25	42.4	10	7	ADE65193	Ade65193 Corticotr
37	25	42.4	10	7	ADE51479	Ade51479 CRF2 non-
38	25	42.4	10	7	ADE51480	Ade51480 CRF2 non-
39	25	42.4	10	7	ADE51475	Ade51475 CRF2 non-
40	25	42.4	10	7	ADE51478	Ade51478 CRF2 non-
41	25	42.4	10	7	ADG84912	Adg84912 Corticotr
42	25	42.4	10	7	ADG84909	Adg84909 Corticotr
43	25	42.4	10	7	ADG84913	Adg84913 Corticotr
44	25	42.4	10	7	ADG84914	Adg84914 Corticotr
45	25	42.4	12	3	AAY66829	Aay66829 T cell an
46	25	42.4	12	8	ADO85928	Ado85928 Linear po
47	25	42.4	15	6	ABO10721	Abo10721 Deimmunis
48	25	42.4	15	6	ABR44665	Abr44665 Murine J4
49	25	42.4	15	8	ADU67921	Adu67921 Mouse ant
50	25	42.4	15	9	AEA46178	Aea46178 Apolipopr
51	25	42.4	15	9	AED41822	Aed41822 Deimmuniz
52	25	42.4	16	4	AAG64402	Aag64402 Human FX
53	25	42.4	18	10	AEF01905	Aef01905 Ii-key/ H
54	25	42.4	18	10	AEF01933	Aef01933 Ii-key/ H
55	25	42.4	18	10	AEF02091	Aef02091 Ii-key/ H
56	25	42.4	20	2	AAR05009	Aar05009 Papilloma
57	25	42.4	20	6	AAE33984	Aae33984 Human apo
58	25	42.4	20	8	ADN00541	Adn00541 Apolipopr
59	25	42.4	20	8	ADM98181	Adm98181 Apolipopr
60	25	42.4	20	10	AEF13617	Aef13617 West Nile
61	24	40.7	9	4	AAU27289	Aau27289 Hepsin pe
62	24	40.7	9	6	ADA17012	Ada17012 Human hep
63	24	40.7	9	7	ADE24992	Ade24992 Human hep
64	24	40.7	9	8	ADP25547	Adp25547 Plasmodiu
65	24	40.7	9	8	ADR18816	Adr18816 HLA B2702
66	24	40.7	10	4	AAB73164	Aab73164 Tumour an
67	24	40.7	10	5	AAU93211	Aau93211 Granulocy
68	24	40.7	10	8	ADR12506	Adr12506 Anti-canc
69	24	40.7	10	8	ADR47113	Adr47113 HLA-bind
70	24	40.7	10	8	ADT90925	Adt90925 Human sur
71	24	40.7	12	2	AAW79554	Aaw79554 Adenoviru
72	24	40.7	12	8	ADQ81421	Adq81421 Negative

73	24	40.7	14	2	AAR76658	Aar76658 Peptide d
74	24	40.7	14	2	AAW18866	Aaw18866 65 kD Glu
75	24	40.7	14	6	ABJ38817	Abj38817 Human G-p
76	24	40.7	14	7	ADW34502	Adw34502 HLA bindi
77	24	40.7	14	7	ADW35735	Adw35735 HLA bindi
78	24	40.7	15	2	AAW12406	Aaw12406 GAD65 res
79	24	40.7	15	5	ABP52861	Abp52861 HIV-1 gp1
80	24	40.7	15	7	ADM08316	Adm08316 Canine im
81	24	40.7	15	7	ADM08393	Adm08393 Canine im
82	24	40.7	15	8	ADT40191	Adt40191 hSARS vir
83	24	40.7	15	8	ADS79608	Ads79608 SARS viru
84	24	40.7	15	8	ADT37721	Adt37721 hSARS vir
85	24	40.7	15	9	ADX25423	Adx25423 Human pro
86	24	40.7	15	9	ADX25366	Adx25366 Human pro
87	24	40.7	15	9	ADX25416	Adx25416 Human pro
88	24	40.7	15	9	ADX25056	Adx25056 Human pro
89	24	40.7	15	9	ADX25364	Adx25364 Human pro
90	24	40.7	15	9	ADX25181	Adx25181 Human pro
91	24	40.7	15	9	ADX25365	Adx25365 Human pro
92	24	40.7	15	9	ADX25111	Adx25111 Human pro
93	24	40.7	15	9	AEA45876	Aea45876 Apolipopr
94	24	40.7	16	2	AAR54015	Aar54015 P-glycopr
95	24	40.7	16	3	AYY58810	Aay58810 Aggrecan
96	24	40.7	16	6	ABB99482	Abb99482 Amino aci
97	24	40.7	16	10	AEF33372	Aef33372 Human cor
98	24	40.7	18	1	AAP60135	Aap60135 Synthetic
99	24	40.7	18	2	AAR14198	Aar14198 Polio-vir
100	24	40.7	18	3	AYY70624	Aay70624 Maize Rac

ALIGNMENTS

RESULT 1

ADY73917

ID ADY73917 standard; peptide; 12 AA.

XX

AC ADY73917;

XX

DT 02-JUN-2005 (first entry)

XX

DE Transmissible spongiform encephalopathy treating peptide, SEQ ID 1.

XX

KW transmissible spongiform encephalopathy; cerebroprotective;

KW neuroprotective; Creutzfeldt Jakob disease; CJD; kuru;

KW Gerstmann-Sträussler-Scheinker syndrome; insomnia; BSE; scrapie.

XX

OS Synthetic.

XX

PN WO2005023285-A2.

XX

PD 17-MAR-2005.

XX

PF 04-AUG-2004; 2004WO-DE001738.

XX

PR 29-AUG-2003; 2003DE-01040260.

XX

PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.

XX

PI Willbold D, Smolinski J, Haenel KO, Wolff MA, Riesner D, Korth C;

XX

DR WPI; 2005-233195/24.

XX

PT Agent for treating spongiform encephalopathy e.g. Jacob Creutzfeldt
PT syndrome, kuru, and Gerstmann-Straeussler-Scheinker syndrome, uses
PT peptides and/or nucleotide sequences coding for the peptides.

XX

PS Claim 1; SEQ ID NO 1; 33pp; German.

XX

CC The invention relates to a novel agent for the treatment or prevention of
CC transmissible spongiform encephalopathy (TSE) by using peptides and/or
CC nucleotide sequences coding for the peptides. The invention further
CC comprises: preparation of an agent as above; use of the peptides in for
CC manufacturing a medicament; treating or preventing transmissible
CC spongiform encephalopathy (TSE), comprising administering an agent as
CC above and/or the nucleic acids. The TSE treating agent has
CC neuroprotective activity. The agent can be used for treating or
CC preventing TSE, e.g. Creutzfeldt Jakob disease in humans, kuru, Gerstmann
CC -Straeussler-Scheinker syndrome, fatal familial insomnia (FFI), BSE in
CC cattle, scrapie in sheep and chronic wasting diseases (CWD) in wild
CC animals. This sequence represents one of the novel peptides used in the
CC TSE treating agent of the invention.

XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 59; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

Qy 1 LKATTNSKLMYY 12
| | | | | | | | | |
Db 1 LKATTNSKLMYY 12

RESULT 2

AAW73902

ID AAW73902 standard; peptide; 15 AA.

XX

AC AAW73902;

XX

DT 17-OCT-2003 (revised)

DT 12-APR-1999 (first entry)

XX

DE B. forsythus protease fragment.

XX

KW Protease; haemolytic activity; diagnosis; periodontosis.

XX

OS Tannerella forsythensis.

XX

PN JP11009284-A.

XX

PD 19-JAN-1999.

XX

PF 25-JUN-1997; 97JP-00185849.

XX

PR 25-JUN-1997; 97JP-00185849.

XX

PA (SUNZ) SUNSTAR CHEM IND CO LTD.

XX

DR WPI; 1999-145900/13.

XX

PT New protease gene derived from Bacteroides forsythus - useful for
PT diagnosis and treatment of periodontosis.
XX
PS Disclosure; Page 13; 13pp; Japanese.
XX
CC This sequence is a fragment of the Bacteroides forsythus protease of the
CC invention. The protein has protease activity and haemolytic activity. The
CC DNA and the polypeptide are useful for diagnosis, treatment and research
CC of periodontosis. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 15 AA;

Query Match 49.2%; Score 29; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps
0;

Qy 4 TTNSKLM 10
| |||||
Db 4 TNNSKLM 10

RESULT 3
ADO34138
ID ADO34138 standard; peptide; 9 AA.
XX
AC ADO34138;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human CLA2 HLA-A1 restricted peptide, SEQ ID 101.
XX
KW Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome 5p14;
KW proliferative disorder; tumour; cancer; carcinoma; dysplasia.
XX
OS Homo sapiens.
XX
PN EP1426442-A1.
XX
PD 09-JUN-2004.
XX
PF 02-DEC-2002; 2002EP-00026772.
XX
PR 02-DEC-2002; 2002EP-00026772.
XX
PA (MTMM-) MTM LAB AG.
XX
PI Hipfel R;
XX
DR WPI; 2004-422595/40.
XX
PT New isolated colorectal lesion associated nucleic acid molecule useful in
PT the detection and therapy of proliferative disorders.
XX
PS Disclosure; SEQ ID NO 101; 123pp; English.
XX
CC The present invention relates to the human Colorectal Lesion Associated 2
CC (CLA2) gene (I; ADO34038), which is located on chromosome 5p14. CLA2
CC sequences are useful for the detection and treatment of proliferative
CC disorders such as: a benign and malignant tumour (head, neck, respiratory
CC tract, gastrointestinal tract, skin and its appendages, central and

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OM protein - protein search, using sw model

Run on: November 2, 2006, 09:44:20 ; Search time 51 Seconds
(without alignments)
20.595 Million cell updates/sec

Title: US-10-570-233-1
Perfect score: 59
Sequence: 1 LKATTNSKLMMY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 287144

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	30	50.8	13	1	US-07-732-114A-13	Sequence 13, Appl
2	30	50.8	13	1	US-08-170-114A-13	Sequence 13, Appl
3	28	47.5	18	1	US-07-995-503A-9	Sequence 9, Appli
4	28	47.5	18	1	US-08-390-510-9	Sequence 9, Appli
5	28	47.5	18	1	US-08-390-790-9	Sequence 9, Appli
6	28	47.5	18	1	US-08-390-509-9	Sequence 9, Appli
7	28	47.5	18	2	US-09-149-860A-9	Sequence 9, Appli
8	27	45.8	16	1	US-08-294-770A-12	Sequence 12, Appl
9	27	45.8	16	1	US-08-448-735C-12	Sequence 12, Appl
10	26	44.1	18	2	US-08-637-670-42	Sequence 42, Appl
11	26	44.1	19	2	US-09-011-143-10	Sequence 10, Appl
12	26	44.1	19	2	US-09-302-495-10	Sequence 10, Appl
13	26	44.1	19	2	US-10-079-616-10	Sequence 10, Appl
14	25	42.4	9	3	US-09-641-528B-332	Sequence 332, App

15	25	42.4	9	3	US-09-641-528B-12506	Sequence 12506, A
16	25	42.4	9	3	US-09-641-528B-20916	Sequence 20916, A
17	25	42.4	9	3	US-09-641-528B-30555	Sequence 30555, A
18	25	42.4	9	3	US-09-641-528B-32701	Sequence 32701, A
19	25	42.4	9	3	US-09-641-528B-40624	Sequence 40624, A
20	25	42.4	10	2	US-10-317-252B-492	Sequence 492, App
21	25	42.4	10	2	US-10-317-252B-495	Sequence 495, App
22	25	42.4	10	2	US-10-317-252B-496	Sequence 496, App
23	25	42.4	10	2	US-10-317-252B-497	Sequence 497, App
24	25	42.4	10	3	US-09-641-528B-282	Sequence 282, App
25	25	42.4	10	3	US-09-641-528B-12390	Sequence 12390, A
26	25	42.4	10	3	US-09-641-528B-20805	Sequence 20805, A
27	25	42.4	10	3	US-09-641-528B-30529	Sequence 30529, A
28	25	42.4	10	3	US-09-641-528B-32548	Sequence 32548, A
29	25	42.4	10	3	US-09-641-528B-40533	Sequence 40533, A
30	25	42.4	11	3	US-09-641-528B-271	Sequence 271, App
31	25	42.4	11	3	US-09-641-528B-12360	Sequence 12360, A
32	25	42.4	11	3	US-09-641-528B-25219	Sequence 25219, A
33	25	42.4	11	3	US-09-641-528B-32505	Sequence 32505, A
34	25	42.4	11	3	US-09-641-528B-40501	Sequence 40501, A
35	25	42.4	15	3	US-09-641-528B-46646	Sequence 46646, A
36	25	42.4	20	1	US-07-678-974D-52	Sequence 52, Appl
37	25	42.4	20	1	US-08-945-168-58	Sequence 58, Appl
38	24	40.7	8	3	US-09-641-528B-4037	Sequence 4037, Ap
39	24	40.7	8	3	US-09-641-528B-9995	Sequence 9995, Ap
40	24	40.7	8	3	US-09-641-528B-21330	Sequence 21330, A
41	24	40.7	8	3	US-09-641-528B-33637	Sequence 33637, A
42	24	40.7	8	3	US-09-641-528B-33851	Sequence 33851, A
43	24	40.7	8	3	US-09-641-528B-41386	Sequence 41386, A
44	24	40.7	9	2	US-09-510-738A-155	Sequence 155, App
45	24	40.7	9	2	US-09-861-966-155	Sequence 155, App
46	24	40.7	9	2	US-09-919-048-155	Sequence 155, App
47	24	40.7	9	2	US-10-102-283-155	Sequence 155, App
48	24	40.7	9	3	US-09-641-528B-4240	Sequence 4240, Ap
49	24	40.7	9	3	US-09-641-528B-9953	Sequence 9953, Ap
50	24	40.7	9	3	US-09-641-528B-21427	Sequence 21427, A
51	24	40.7	9	3	US-09-641-528B-33638	Sequence 33638, A
52	24	40.7	9	3	US-09-641-528B-33898	Sequence 33898, A
53	24	40.7	9	3	US-09-641-528B-41241	Sequence 41241, A
54	24	40.7	9	3	US-09-641-528B-51375	Sequence 51375, A
55	24	40.7	10	2	US-09-620-091-24	Sequence 24, Appl
56	24	40.7	10	3	US-09-641-528B-9954	Sequence 9954, Ap
57	24	40.7	10	3	US-09-641-528B-10008	Sequence 10008, A
58	24	40.7	10	3	US-09-641-528B-10009	Sequence 10009, A
59	24	40.7	10	3	US-09-641-528B-21407	Sequence 21407, A
60	24	40.7	10	3	US-09-641-528B-33639	Sequence 33639, A
61	24	40.7	10	3	US-09-641-528B-33852	Sequence 33852, A
62	24	40.7	10	3	US-09-641-528B-33897	Sequence 33897, A
63	24	40.7	10	3	US-09-641-528B-33899	Sequence 33899, A
64	24	40.7	10	3	US-09-641-528B-41242	Sequence 41242, A
65	24	40.7	10	3	US-09-641-528B-41412	Sequence 41412, A
66	24	40.7	10	3	US-09-641-528B-41413	Sequence 41413, A
67	24	40.7	11	3	US-09-641-528B-4038	Sequence 4038, Ap
68	24	40.7	11	3	US-09-641-528B-9996	Sequence 9996, Ap
69	24	40.7	11	3	US-09-641-528B-10004	Sequence 10004, A
70	24	40.7	11	3	US-09-641-528B-10010	Sequence 10010, A
71	24	40.7	11	3	US-09-641-528B-16999	Sequence 16999, A
72	24	40.7	11	3	US-09-641-528B-21331	Sequence 21331, A
73	24	40.7	11	3	US-09-641-528B-26024	Sequence 26024, A
74	24	40.7	11	3	US-09-641-528B-33853	Sequence 33853, A
75	24	40.7	11	3	US-09-641-528B-33888	Sequence 33888, A

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OM protein - protein search, using sw model

Run on: November 2, 2006, 09:45:05 ; Search time 183 Seconds
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Title: US-10-570-233-1

Perfect score: 59

Sequence: 1 LKATTNSKLMMY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 460792

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

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SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	28	47.5	18	3	US-09-836-861-9	Sequence 9, Appl
2	27	45.8	14	5	US-10-833-951-112	Sequence 112, App
3	27	45.8	15	5	US-10-660-370-54	Sequence 54, Appl
4	27	45.8	19	3	US-09-864-761-39115	Sequence 39115, A
5	27	45.8	20	6	US-11-075-234-289	Sequence 289, App
6	26	44.1	12	4	US-10-649-873-127	Sequence 127, App
7	26	44.1	12	5	US-10-821-283-17	Sequence 17, Appl
8	26	44.1	13	4	US-10-308-393-50	Sequence 50, Appl
9	26	44.1	13	5	US-10-948-707-928	Sequence 928, App
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11	26	44.1	15	5	US-10-660-370-73	Sequence 73, Appl
12	26	44.1	19	4	US-10-079-616-10	Sequence 10, Appl
13	26	44.1	19	4	US-10-324-143-118	Sequence 118, App
14	25	42.4	10	4	US-10-315-964A-492	Sequence 492, App
15	25	42.4	10	4	US-10-315-964A-495	Sequence 495, App

16	25	42.4	10	4	US-10-315-964A-496	Sequence 496, App
17	25	42.4	10	4	US-10-315-964A-497	Sequence 497, App
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24	25	42.4	10	4	US-10-317-252A-496	Sequence 496, App
25	25	42.4	10	4	US-10-317-252A-497	Sequence 497, App
26	25	42.4	10	6	US-11-121-612-492	Sequence 492, App
27	25	42.4	10	6	US-11-121-612-495	Sequence 495, App
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33	25	42.4	15	4	US-10-160-506-42	Sequence 42, Appl
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35	25	42.4	15	4	US-10-688-015-42	Sequence 42, Appl
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46	24	40.7	9	4	US-10-652-993-155	Sequence 155, App
47	24	40.7	9	6	US-11-004-399-3558	Sequence 3558, Ap
48	24	40.7	10	4	US-10-715-417-59	Sequence 59, Appl
49	24	40.7	10	4	US-10-354-090-59	Sequence 59, Appl
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51	24	40.7	10	5	US-10-929-988-24	Sequence 24, Appl
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53	24	40.7	13	4	US-10-456-097-19	Sequence 19, Appl
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56	24	40.7	14	5	US-10-833-951-97	Sequence 97, Appl
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58	24	40.7	15	4	US-10-327-598-282	Sequence 282, App
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68	24	40.7	15	5	US-10-857-484-6391	Sequence 6391, Ap
69	24	40.7	15	5	US-10-857-484-6398	Sequence 6398, Ap
70	24	40.7	15	6	US-11-004-399-1872	Sequence 1872, Ap
71	24	40.7	16	5	US-10-895-064-1958	Sequence 1958, Ap
72	24	40.7	16	6	US-11-059-633-2	Sequence 2, Appli
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76	24	40.7	19	6	US-11-059-633-24	Sequence 24, Appl

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OM protein - protein search, using sw model

Run on: November 2, 2006, 09:39:19 ; Search time 39 Seconds
(without alignments)
29.605 Million cell updates/sec

Title: US-10-570-233-1
Perfect score: 59
Sequence: 1 LKATTNSKLMMY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*

1: pirl:*

2: pir2:*

3: pir3:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	37.3	17	4	I76673	hypothetical COII/
3	22	37.3	19	2	S01203	patatin (clone LPO
4	21	35.6	11	2	PH1375	T antigen variant
5	21	35.6	11	2	PH1376	T antigen variant
6	21	35.6	20	2	A47105	dystroglycan - chi
7	20	33.9	13	2	PH0138	T-cell receptor be
8	20	33.9	15	2	PH0782	T-cell receptor al
9	20	33.9	16	2	H49039	T-cell receptor be
10	20	33.9	16	2	G24687	T-cell receptor be
11	20	33.9	16	2	C44896	heat shock protein
12	20	33.9	17	2	A27486	follitropin inhibi
13	20	33.9	18	2	B48839	T-cell receptor be
14	20	33.9	19	2	S78411	ribosomal protein
15	20	33.9	20	2	B53875	creatine kinase (E
16	20	33.9	20	2	S56756	link protein - rat
17	20	33.9	20	2	A61526	major milk gland p

18	20	33.9	20	2	PC4384	DnaK protein homol
19	19	32.2	9	2	A28924	fructose-bisphosph
20	19	32.2	10	2	PH0894	T-cell receptor be
21	19	32.2	15	2	PH0797	T-cell receptor al
22	19	32.2	15	2	E49037	TcR delta chain V-
23	19	32.2	20	2	S38763	S-adenosyl-L-methi
24	18	30.5	10	2	S74176	gluconokinase (EC
25	18	30.5	13	2	S57567	T cell receptor V-
26	18	30.5	14	2	PH0801	T-cell receptor al
27	18	30.5	16	2	A27803	myosin light chain
28	18	30.5	16	2	PH0766	T-cell receptor be
29	18	30.5	16	2	S35627	uvxS protein - pha
30	18	30.5	17	2	I49593	cystic fibrosis tr
31	18	30.5	17	2	I84733	gene CTR protein
32	18	30.5	17	2	PH1312	Ig heavy chain DJ
33	18	30.5	18	2	S48862	murine cyclin H -
34	18	30.5	19	2	A49725	valine-tRNA ligase
35	17	28.8	9	2	PC7076	spectrin alpha cha
36	17	28.8	12	2	PT0216	T-cell receptor be
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38	17	28.8	12	4	S49073	frame shifted cyta
39	17	28.8	13	2	S12388	argA protein - Sal
40	17	28.8	14	2	PH0795	T-cell receptor al
41	17	28.8	15	2	PH1631	Ig H chain V-D-J r
42	17	28.8	16	2	A49255	T-cell receptor be
43	17	28.8	16	2	PH1477	T-cell receptor be
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46	17	28.8	16	2	S02473	coat protein VP1 -
47	17	28.8	17	2	A34835	ribosomal protein
48	17	28.8	17	2	PC4383	DnaK protein homol
49	17	28.8	17	2	PT0234	Ig heavy chain CRD
50	17	28.8	17	2	PH1340	Ig heavy chain DJ
51	17	28.8	17	2	S58129	hypothetical prote
52	17	28.8	18	2	B27504	histone H2B - mous
53	17	28.8	19	2	S57558	T cell receptor V-
54	17	28.8	19	2	S11611	ribosomal protein
55	17	28.8	20	2	S02002	photosystem II pro
56	17	28.8	20	2	S20276	18K protein - Rhod
57	17	28.8	20	2	S15861	estrogen receptor
58	17	28.8	20	2	PQ0046	citrate (si)-synth
59	17	28.8	20	2	S27351	lysophospholipase
60	16	27.1	6	2	I49424	cytotoxic T-lympho
61	16	27.1	10	2	I36893	apolipoprotein A-I
62	16	27.1	10	2	C30572	T-cell receptor be
63	16	27.1	10	2	A24407	amicyanin - Paraco
64	16	27.1	11	2	PC4267	ribosomal protein
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75	16	27.1	14	1	LFEBWC	trp operon leader
76	16	27.1	14	2	S62374	alpha-1-antichymot
77	16	27.1	14	2	PH1768	T cell receptor al
78	16	27.1	14	2	PH1628	Ig H chain V-D-J r

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OM protein - protein search, using sw model

Run on: November 2, 2006, 09:45:59 ; Search time 41 Seconds
(without alignments)
24.511 Million cell updates/sec

Title: US-10-570-233-1
Perfect score: 59
Sequence: 1 LKATTNSKLMMY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 320231 seqs, 83745634 residues

Total number of hits satisfying chosen parameters: 56157

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	26	44.1	20	7	US-11-134-871-2964	Sequence 2964, Ap
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5	25	42.4	15	7	US-11-219-563-42	Sequence 42, Appl
6	24	40.7	9	6	US-10-537-642-124	Sequence 124, App
7	24	40.7	14	7	US-11-397-759-35	Sequence 35, Appl
8	24	40.7	16	7	US-11-342-706-25	Sequence 25, Appl
9	24	40.7	16	7	US-11-274-885-2	Sequence 2, Appli
10	24	40.7	19	7	US-11-274-885-24	Sequence 24, Appl
11	24	40.7	20	7	US-11-134-871-2054	Sequence 2054, Ap
12	24	40.7	20	7	US-11-134-871-2851	Sequence 2851, Ap
13	23.5	39.8	15	7	US-11-417-625-29	Sequence 29, Appl

14	23	39.0	9	6	US-10-537-642-89	Sequence 89, Appl
15	23	39.0	15	7	US-11-143-737-19	Sequence 19, Appl
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17	23	39.0	18	7	US-11-064-109-33	Sequence 33, Appl
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19	22	37.3	8	7	US-11-367-915-7	Sequence 7, Appl
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21	22	37.3	11	7	US-11-301-314-6	Sequence 6, Appl
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23	22	37.3	14	7	US-11-436-610-45	Sequence 45, Appl
24	22	37.3	15	7	US-11-295-192A-691	Sequence 691, App
25	22	37.3	15	7	US-11-295-192A-692	Sequence 692, App
26	22	37.3	15	7	US-11-295-192A-693	Sequence 693, App
27	22	37.3	15	7	US-11-295-192A-694	Sequence 694, App
28	22	37.3	15	7	US-11-410-610-61	Sequence 61, Appl
29	22	37.3	16	7	US-11-134-871-160	Sequence 160, App
30	22	37.3	17	7	US-11-343-271-64	Sequence 64, Appl
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33	21	35.6	9	6	US-10-537-642-851	Sequence 851, App
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35	21	35.6	11	7	US-11-436-610-25	Sequence 25, Appl
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37	21	35.6	13	7	US-11-353-459-135	Sequence 135, App
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40	21	35.6	13	7	US-11-353-459-345	Sequence 345, App
41	21	35.6	13	7	US-11-376-695-1222	Sequence 1222, Ap
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51	20	33.9	9	7	US-11-376-695-107	Sequence 107, App
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54	20	33.9	13	6	US-10-967-088-59	Sequence 59, Appl
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73	20	33.9	17	7	US-11-094-132-55	Sequence 55, Appl
74	20	33.9	17	7	US-11-134-871-3367	Sequence 3367, Ap

75	20	33.9	17	7	US-11-134-871-3501	Sequence 3501, Ap
76	20	33.9	18	7	US-11-134-871-715	Sequence 715, App
77	20	33.9	18	7	US-11-134-871-1561	Sequence 1561, Ap
78	20	33.9	18	7	US-11-134-871-2939	Sequence 2939, Ap
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80	20	33.9	19	7	US-11-134-871-3104	Sequence 3104, Ap
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86	19	32.2	10	6	US-10-526-062-24	Sequence 24, Appl
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88	19	32.2	11	7	US-11-134-871-2771	Sequence 2771, Ap
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97	19	32.2	14	6	US-10-527-603-60	Sequence 60, Appl
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ALIGNMENTS

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US-11-411-832-17

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; Publication No. US20060210573A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/11/411,832
; CURRENT FILING DATE: 2006-04-27
; PRIOR APPLICATION NUMBER: US/10/821,283
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal
antibody
US-11-411-832-17
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Query Match 44.1%; Score 26; DB 7; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps
0;

Qy 5 TNSKLM 10
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Db 5 TNTKLM 10

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; Publication No. US20060234909A1
; GENERAL INFORMATION:
; APPLICANT: Ballatore, Carlo
; APPLICANT: Castellino, Angelo
; APPLICANT: Desharnais, Joel
; APPLICANT: Guo, Zijian
; APPLICANT: Li, Qing
; APPLICANT: Newman, Michael James
; APPLICANT: Sun, Chengzao
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: DRUG EFFICIENCY
; FILE REFERENCE: 11685-0009-999
; CURRENT APPLICATION NUMBER: US/11/376,695
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/948,707
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 60/505,325
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: 60/568,340
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/581,835
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 1422
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 928
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo Sapiens

US-11-376-695-928

Query Match 44.1%; Score 26; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps
0;

Qy 1 LKATTNSKL 9
|| ||:| |
Db 2 LKGTTHSLL 10

RESULT 3

US-11-134-871-2964
; Sequence 2964, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 2, 2006, 09:35:55 ; Search time 297 Seconds
(without alignments)
37.374 Million cell updates/sec

Title: US-10-570-233-1
Perfect score: 59
Sequence: 1 LKATTNSKLMMY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 16145

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	42.4	10	2	P82224_BOMMO	P82224 bombyx mori
2	25	42.4	16	2	Q3ZEY0_9CHAR	Q3zey0 actitis hyp
3	24	40.7	13	2	Q35793_YEAST	Q35793 saccharomyces
4	23	39.0	20	2	Q41475_SOLTU	Q41475 solanum tub
5	22	37.3	10	2	P82223_BOMMO	P82223 bombyx mori
6	22	37.3	13	2	Q42373_SOLTU	Q42373 solanum tub
7	22	37.3	16	2	Q3ZEV7_9CHAR	Q3zev7 tringa stag
8	22	37.3	18	2	Q4YR78_PLABE	Q4yr78 plasmodium
9	22	37.3	18	2	Q7RMW9_PLAYO	Q7rmw9 plasmodium
10	22	37.3	19	2	Q41466_SOLTU	Q41466 solanum tub
11	22	37.3	19	2	Q41471_SOLTU	Q41471 solanum tub
12	22	37.3	19	2	Q9R4B9_STRSP	Q9r4b9 streptococcus
13	22	37.3	20	2	Q41468_SOLTU	Q41468 solanum tub
14	22	37.3	20	2	Q41469_SOLTU	Q41469 solanum tub
15	21	35.6	12	2	P82334_PEA	P82334 pisum sativ
16	21	35.6	13	2	Q7SCD5_NEUCR	Q7scd5 neurospora
17	21	35.6	13	2	Q9ZEZ1_9ENTR	Q9zez1 buchnera ap
18	21	35.6	16	2	Q75MY2_HUMAN	Q75my2 homo sapien
19	21	35.6	16	2	Q6JDH9_CANFA	Q6jdh9 canis famil

20	21	35.6	17	1	ALYS_MYCPH	P81528 mycobacteri
21	21	35.6	19	2	Q4X4T2_PLACH	Q4x4t2 plasmodium
22	21	35.6	20	2	Q7DMV0_SOLTU	Q7dmv0 solanum tub
23	21	35.6	20	2	Q9PRM4_CHICK	Q9prm4 gallus gall
24	21	35.6	20	2	Q9PS38_RANCA	Q9ps38 rana catesb
25	20	33.9	10	2	Q8VIL8_MOUSE	Q8vil8 mus musculu
26	20	33.9	11	2	Q9R790_BORGA	Q9r790 borrelia ga
27	20	33.9	12	2	Q5DU72_PIG	Q5du72 sus scrofa
28	20	33.9	12	2	Q56QW1_9PHAE	Q56qw1 undaria pin
29	20	33.9	14	2	Q9MRF6_9POAL	Q9mrf6 hordeum mur
30	20	33.9	15	1	DNAK_COMAC	P83709 comamonas a
31	20	33.9	15	2	O05463_9PROT	O05463 nitrosospir
32	20	33.9	15	2	P97249_9PROT	P97249 nitrosospir
33	20	33.9	15	2	Q9QVA9_9MURI	Q9qva9 rattus sp.
34	20	33.9	16	1	FIBA_VULVU	P68212 vulpes vulp
35	20	33.9	16	2	Q9S898_LYCES	Q9s898 lycopersico
36	20	33.9	17	2	Q9UML8_HUMAN	Q9uml8 homo sapien
37	20	33.9	17	2	Q4X4S0_PLACH	Q4x4s0 plasmodium
38	20	33.9	17	2	Q7M2M4_BOVIN	Q7m2m4 bos taurus
39	20	33.9	17	2	Q6PUY6_9HEPC	Q6puy6 hepatitis c
40	20	33.9	18	1	PH1_PERAM	P82694 periplaneta
41	20	33.9	18	2	Q5EBR8_HUMAN	Q5ebr8 homo sapien
42	20	33.9	18	2	O46665_MACRO	O46665 macropus ro
43	20	33.9	18	2	P79435_HYLLA	P79435 hylobates l
44	20	33.9	18	2	Q7JFI7_MACFA	Q7jfi7 macaca fasc
45	20	33.9	18	2	Q7JFI8_SAISC	Q7jfi8 saimiri sci
46	20	33.9	18	2	Q7JFI9_BOVIN	Q7jfi9 bos taurus
47	20	33.9	18	2	Q65ZT5_BORGA	Q65zt5 borrelia ga
48	20	33.9	19	2	Q4XQY2_PLACH	Q4xqy2 plasmodium
49	20	33.9	19	2	P97555_RAT	P97555 rattus norv
50	20	33.9	20	1	DNAK_CLOPA	P81341 clostridium
51	20	33.9	20	1	DNAK_NAEFO	P83724 naegleria f
52	20	33.9	20	1	DNAK_THIFE	P29133 thiobacillu
53	20	33.9	20	2	Q4XB58_PLACH	Q4xb58 plasmodium
54	20	33.9	20	2	Q4XK96_PLACH	Q4xk96 plasmodium
55	20	33.9	20	2	Q7M1A4_ACISP	Q7m1a4 acinetobact
56	20	33.9	20	2	Q9PSI4_ONCKI	Q9psi4 oncorhynchu
57	19.5	33.1	16	2	Q4YSC2_PLABE	Q4ysc2 plasmodium
58	19	32.2	9	2	Q7M2K6_RABIT	Q7m2k6 oryctolagus
59	19	32.2	11	2	Q9L4F7_BACCE	Q914f7 bacillus ce
60	19	32.2	11	2	Q7Y9B6_9SAUR	Q7y9b6 amphiboluru
61	19	32.2	11	2	Q7Y9D1_9SAUR	Q7y9d1 typanocryp
62	19	32.2	11	2	Q9G679_HYPDL	Q9g679 hypsilurus
63	19	32.2	12	2	Q7RH59_PLAYO	Q7rh59 plasmodium
64	19	32.2	12	2	Q9TTE3_PIG	Q9tte3 sus scrofa
65	19	32.2	13	1	FRI2_PEA	P83445 pisum sativ
66	19	32.2	13	2	Q9SB03_ORYSA	Q9sb03 oryza sativ
67	19	32.2	15	2	Q9UCE5_HUMAN	Q9uce5 homo sapien
68	19	32.2	16	2	Q6Y662_MYCML	Q6y662 mycoplasma
69	19	32.2	16	2	Q765Z2_CHICK	Q765z2 gallus gall
70	19	32.2	16	2	Q9PSL6_CHICK	Q9psl6 gallus gall
71	19	32.2	17	2	Q75I46_ORYSA	Q75i46 oryza sativ
72	19	32.2	18	2	Q5BY25_SCHJA	Q5by25 schistosoma
73	19	32.2	19	1	DCAM_ACACA	P34039 acanthamoeb
74	19	32.2	19	1	PHLC_STAIN	P80924 staphylococ
75	19	32.2	19	2	Q2TD78_9HYME	Q2td78 solenopsis
76	19	32.2	19	2	Q4Y2D0_PLACH	Q4y2d0 plasmodium
77	19	32.2	19	2	Q4YLL6_PLABE	Q4yll6 plasmodium
78	19	32.2	19	2	Q5C169_SCHJA	Q5c169 schistosoma
79	19	32.2	19	2	Q9TWH8_PARCM	Q9twh8 paralithode
80	19	32.2	20	2	Q2LH17_9NEOP	Q2lh17 panesthia a

81	19	32.2	20	2	P79837_PRIBE	P79837 prionailuru
82	19	32.2	20	2	Q42486_SOLTU	Q42486 solanum tub
83	19	32.2	20	2	Q47598_ECOLI	Q47598 escherichia
84	19	32.2	20	2	Q56130_SALTY	Q56130 salmonella
85	19	32.2	20	2	Q9K2Y9_MYCMC	Q9k2y9 mycoplasma
86	19	32.2	20	2	Q9K2Z0_MYCMC	Q9k2z0 mycoplasma
87	19	32.2	20	2	Q9KJP4_MYCMS	Q9kjp4 mycoplasma
88	19	32.2	20	2	Q9KJP5_MYCML	Q9kjp5 mycoplasma
89	19	32.2	20	2	Q9KJQ1_MYCML	Q9kjq1 mycoplasma
90	19	32.2	20	2	Q9KJQ2_MYCCA	Q9kjq2 mycoplasma
91	19	32.2	20	2	Q9KJQ6_MYCCC	Q9kjq6 mycoplasma
92	19	32.2	20	2	Q9KJQ8_9MOLU	Q9kjq8 mycoplasma
93	19	32.2	20	2	Q9KJR1_9MOLU	Q9kjr1 mycoplasma
94	19	32.2	20	2	Q9KJR2_9MOLU	Q9kjr2 mycoplasma
95	19	32.2	20	2	Q9R5M5_9NOCA	Q9r5m5 rhodococcus
96	19	32.2	20	2	Q9PRN6_SCYCA	Q9prn6 scyliorhinu
97	18	30.5	11	2	Q4L8Q1_STAHJ	Q4l8q1 staphylococ
98	18	30.5	12	2	Q9YPJ1_9CORO	Q9ypj1 infectious
99	18	30.5	12	2	Q85498_9RETR	Q85498 equine infe
100	18	30.5	12	2	Q8AEW7_9HIV1	Q8aew7 human immun

ALIGNMENTS

RESULT 1

P82224_BOMMO

ID P82224_BOMMO PRELIMINARY; PRT; 10 AA.

AC P82224;

DT 01-OCT-2001, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2001, sequence version 1.

DT 07-FEB-2006, entry version 10.

DE Unknown protein from 2D-page (Fragment).

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;

OC Bombycidae; Bombyx.

OX NCBI_TaxID=7091;

RN [1]

RP PROTEIN SEQUENCE.

RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;

RX MEDLINE=21177481; PubMed=11280994;

RA Zhong B.X.;

RT "Protein database for several tissues derived from five instar of silkworm.";

RL Yi Chuan Xue Bao 28:217-224(2001).

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CC -----

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1064 MW; D77CBF25B1F1B2CD CRC64;

Query Match 42.4%; Score 25; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKATTNSKLM 10
 | | |:||:|:
 Db 1 LPATVTHSKVL 10

RESULT 2

Q3ZEY0_9CHAR

ID Q3ZEY0_9CHAR PRELIMINARY; PRT; 16 AA.

AC Q3ZEY0;

DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.

DT 27-SEP-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE ATP synthase F0 subunit 8 (Fragment).

GN Name=ATP8;

OS Actitis hypoleucus (common sandpiper).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Charadriiformes; Scolopacidae; Actitis.

OX NCBI_TaxID=320702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Pereira S.L., Baker A.J.;

RT "Multiple gene evidence for parallel evolution and retention of ancestral morphological states in the shanks (Charadriiformes: Scolopacidae).";

RL Condor 107:514-526(2005).

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CC -----

DR EMBL; AY894263; AAX93990.1; -; Genomic_DNA.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON_TER 1 1

SQ SEQUENCE 16 AA; 1961 MW; 693F802BC211E86D CRC64;

Query Match 42.4%; Score 25; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 8.6e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps
0;

Qy 2 KATTNSKLM MY 12
| :||:| ::
Db 1 KTSTNTKTTLW 11

RESULT 3

Q35793_YEAST

ID Q35793_YEAST PRELIMINARY; PRT; 13 AA.

AC Q35793;

DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE Inside intron 4 (Fragment).

OS Saccharomyces cerevisiae (Baker's yeast).

OG Mitochondrion.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=D273-10B;

RX MEDLINE=81069885; PubMed=6254986;

RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;